Octet Data Analysis HT Software Version 12

Newest features for advanced Epitope Binning and Quantitation analyses

Key features

- NEW BinChart for convenient binning of antibodies
- Advanced settings for fitting quantitation datasets
- Optimal visualization via overlaid fitted traces on top of raw quantitation binding traces
- NEW capability for reference subtraction within and across plates
- Optimized Report Tab for direct creation of exportable reports

Overview

The Octet® Data Analysis HT software is designed for fast analysis of large datasets from quantitation, kinetic and epitope binning assays. In version 12, the Data Analysis HT software offers faster and more advanced epitope binning and quantitation analysis options.

BinChart

Epitope binning groups a panel of monoclonal antibodies (mAbs) into bins based upon similarities in antigen recognition sites or epitopes. This grouping is performed using cross competition assays, in which the competitive binding of antibody pairs to a specific antigen is characterized. If the binding of antigen to one mAb prevents the binding of another mAb, then these mAbs are considered to bind to similar or overlapping epitopes. If binding of a mAb to the antigen does not interfere with the binding of the other mAb, then they are considered to bind to distinct, non-overlapping epitopes. Two criteria must be fulfilled in order to assign mAbs into the same bin. First, all mAbs in the same bin should block each other’s ability to bind the antigen. Second, all mAbs in the same bin should have similar blocking profiles when paired with other mAbs in the panel.

Version 12 introduces a BinChart feature which assigns screened antibodies to bins based on the binding threshold set during analysis. This binding threshold can be adjusted to analyze varying binning of antibodies as a result of the changing threshold (Figures 1 and 2).

Figure 1: Example BinChart from a 32x64 screen. Each bin represents antibodies that block each other’s ability to bind the antigen, and have similar blocking profiles when paired with other antibodies in the panel. This example was created using a low binding nm threshold setting, which resulted in fewer antibodies within each bin. When the mouse arrow is hovered over a bin, the top of the BinChart window also displays the list of antibodies within that bin.

Figure 2: Example BinChart from a 32x64 screen. Each bin represents antibodies that block each other’s ability to bind the antigen, and have similar blocking profiles when paired with other antibodies in the panel. In this example, a higher binding nm threshold setting was used, which resulted in more antibodies grouped in fewer number of bins compared to Fig 1.
Advanced quantitation

Version 12 adds new fitting model classifiers for advanced users. The model classifiers (Figure 3) help choose the best fit for the binding interactions. Version 12 also provides optimal visualization (Figure 4) by overlaying fitted traces on top of the raw binding traces.

- The Legacy model classifier chooses a fitting model (single exponential, double exponential) based on maximum slope of the raw binding traces.
- The Best Fit model classifier looks to minimize residuals — the difference between raw binding traces and fitted traces. If the difference is zero between different models (single exponential, double exponential), the Best Fit model classifier will choose the simpler of the two models.
- The Single Exponential model classifier forces fitting of raw binding traces with the single exponential mathematical model. This classifier might be best suited for known 1:1 binding interactions.

Report Tab

Take full advantage of the newly optimized Report Tab to create exportable reports with any number of data points. New features add capability to modify and sort data tables, and flexibility for font settings.

Ordering information

<table>
<thead>
<tr>
<th>Part no.</th>
<th>Description</th>
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<tr>
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</tr>
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<td>50-0296</td>
<td>OCTET CFR SOFTWARE V12.X VALIDATION PACKAGE</td>
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Figure 3: A screenshot of the Advanced Settings options for choosing among model classifiers.

Figure 4: In Octet Data Analysis HT software version 12, fitted traces can now be overlaid on raw binding traces for optimal visualization. The Best Fit model classifier was used in this example.